

## SEQUENCE LISTING

<110> Metanomics GmbH & Co. KGaA

<120> Process for preparing amino acids

<130> 2002\_960

<140> PF54195

<141> 2002-12-20

<160> 26

<170> PatentIn version 3.1

<210> 1

<211> 1164

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1164)

<223> Threonine aldolase

<400> 1

atg act gaa ttc gaa ttg cct cca aaa tat atc acc gct gct aac gac  
Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp  
1 5 10 15

48

ttg cgg tca gac aca ttc acc act cca act gca gag atg atg gag gcc  
Leu Arg Ser Asp Thr Phe Thr Pro Thr Ala Glu Met Met Glu Ala  
20 25 30

96

gct tta gag gcc tct atc ggt gac gct gtc tac ggt gaa gat gtt gac  
Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp  
35 40 45

144

acc gtt agg ctc gaa cag acc gtt gcc cgc atg gct ggc aaa gaa gca  
Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala  
50 55 60

192

ggt ttg ttc tgt gtc tct ggg act ttg tcc aac cag att gcc atc aga  
Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg  
65 70 75 80

240

act cac ttg atg caa cct cca tac tct att cta tgt gat tac agg gct Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala 85 90 95	288
cac gtt tac act cac gaa gcc gct gga ctg gcg atc ttg tct caa gcg His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala 100 105 110	336
atg gtg gtt cct gtg gtt cct tcc aac ggt gac tac ttg acc ttg gaa Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu 115 120 125	384
gac atc aag tca cac tac gtc cca gac gac ggt gat att cac ggt gcc Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala 130 135 140	432
ccc acc aga ttg att tct ctg gaa aac act tta cac ggt att gtt tat Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr 145 150 155 160	480
cca ttg gaa gaa ctg gtc cgc atc aaa gct tgg tgt atg gaa aat ggt Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly 165 170 175	528
ctc aaa cta cat tgt gac ggt gcc aga atc tgg aat gcc gct gca caa Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Gln 180 185 190	576
tct ggc gtg cca tta aag caa tat ggg gaa atc ttc gac tcc atc tcc Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser 195 200 205	624
atc tgt cta tcc aag tct atg ggt gct cct att ggg tcc gtc ttg gtt Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val 210 215 220	672
ggg aac ctt aag ttt gtc aag aag gcc acc cat ttc aga aaa caa caa Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln 225 230 235 240	720
ggt ggt ggt att aga caa tct ggt atg atg gct aga atg gct ctt gta Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val 245 250 255	768
aac atc aac aac gat tgg aag tcc caa ttg ctg tac tcg cac tct ttg Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu 260 265 270	816
gct cat gaa tta gcc gaa tat tgt gag gca aag ggc atc ccg cta gag Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu 275 280 285	864
tct cca gca gac acc aac ttt gtc ttt att aac ctg aag gcc gct aga Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg 290 295 300	912
atg gac cca gat gtc ctt gtt aag aag ggt ttg aag tac aac gtt aag Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys 305 310 315 320	960
cta atg ggt ggt aga gtc ttc cac tat caa gtc acc aga gat act Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr 325 330 335	1008

ttg gaa aaa gtc aaa ttg gcc atc tcc gag gcc ttc gac tat gct aaa 1056  
 Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys  
 340 345 350

gaa cat cct ttc gac tgt aac gga cct acc cag att tac cgt agt gaa 1104  
 Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu  
 355 360 365

tcc acc gag gtc gac gtt gat ggc aac gct atc cgc gaa ata aaa acc 1152  
 Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr  
 370 375 380

tac aaa tac tga 1164  
 Tyr Lys Tyr  
 385

<210> 2  
<211> 387  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 2

Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp  
 1 5 10 15

Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala  
 20 25 30

Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp  
 . 35 40 45

Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala  
 50 55 60

Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg  
 65 70 75 80

Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala  
 85 90 95

His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala  
 100 105 110

Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu  
 115 120 125

Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala  
 130 135 140

Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr  
 145 150 155 160

Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly  
 165 170 175

Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Gln  
 180 185 190

**PF 54195**

Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser  
195 200 205

Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val  
210 215 220

Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln  
225 230 235 240

Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val  
245 250 255

Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu  
260 265 270

Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu  
275 280 285

Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg  
290 295 300

Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys  
305 310 315 320

Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr  
325 330 335

Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys  
340 345 350

Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu  
355 360 365

Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr  
370 375 380

Tyr Lys Tyr  
385

<210> 3  
<211> 376  
<212> PRT  
<213> Canola

<400> 3

Gly Cys Phe Ala Cys Tyr Leu Val Gly Gly Phe Ser Val Gln Glu Lys  
1 5 10 15

Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro  
20 25 30

Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp  
35 40 45

Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala  
50 55 60

Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met

65	70	75	80
Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu			
85	90		95
Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly			
100	105		110
Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp			
115	120		125
Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro			
130	135		140
Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn			
145	150		155
160			
Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp			
165	170		175
Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp			
180	185		190
Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp			
195	200		205
Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly			
210	215		220
Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile			
225	230		235
240			
Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Met Arg Gln			
245	250		255
Ile Gly Leu Leu Cys Ala Ala Leu Val Ala Leu Gln Glu Asn Val			
260	265		270
Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly			
275	280		285
Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr			
290	295		300
Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu			
305	310		315
320			
Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu			
325	330		335
Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser			
340	345		350
Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys			
355	360		365
Gly Val Gln Lys Glu Met Gly Asn			
370	375		

**PF 54195**

<210> 4  
<211> 115  
<212> PRT  
<213> Soybean

<400> 4

Leu Phe Gly Leu Leu Ala Ile Leu Leu Glu Tyr Leu Glu Lys Met Val  
1 5 10 15

Pro Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro Ser Glu  
20 25 30

Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp Val Leu  
35 40 45

Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile  
50 55 60

Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn  
65 70 75 80

Leu Ile Ser Val Leu Val His Cys Asp Ile Arg Gly Ser Glu Val Ile  
85 90 95

Leu Gly Asp Asn Ser His Ile His Ile Tyr Glu Asn Gly Gly Ile Ala  
100 105 110

Thr Leu Gly  
115

<210> 5  
<211> 127  
<212> PRT  
<213> Rice

<220>

<221> misc\_feature

<222> (1)..(127)

<223> unknown or other

<400> 5

Lys Thr Leu Xaa Gly Gly Met Arg Gln Val Gly Ile Leu Cys Ala Ala  
1 5 10 15

Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Gln Ser Asp His  
20 25 30

Asn Lys Ala Lys Leu Leu Ala Asp Gly Leu Asn Glu Ile Lys Gly Leu  
35 40 45

**PF 54195**

Arg Val Asp Ile Ser Ser Val Glu Thr Asn Ile Ile Tyr Val Glu Val  
50 55 60

Glu Glu Gly Ser Arg Ala Thr Ala Ala Lys Leu Cys Lys Asp Leu Glu  
65 70 75 80

Asp Tyr Gly Ile Leu Leu Met Pro Met Gly Ser Ser Arg Leu Arg Ile  
85 90 95

Val Phe His His Gln Ile Ser Ala Ser Asp Val Gln Tyr Ala Leu Ser  
100 105 110

Cys Phe Gln Gln Ala Val Asn Gly Val Arg Asn Glu Asn Gly Asn  
115 120 125

<210> 6  
<211> 147  
<212> PRT  
<213> Rice

<400> 6

Gly Arg Arg Phe Arg Ala Ile Arg Asp Pro Met Gly Glu Leu Phe Tyr  
1 5 10 15

Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn Thr His Ala Asn Ser Gly  
20 25 30

Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp Arg Val Gly Glu Leu Ala  
35 40 45

Lys Lys His Gly Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn  
50 55 60

Ala Ser Val Ala Leu Gly Val Pro Val Asp Arg Leu Val Gln Ala Ala  
65 70 75 80

Asp Ser Val Ser Val Cys Leu Ser Lys Gly Ile Gly Ala Pro Val Gly  
85 90 95

Ser Val Ile Val Gly Ser Lys Asn Phe Ile Ala Lys Ala Arg Arg Leu  
100 105 110

Arg Lys Thr Leu Gly Gly Met Arg Gln Ile Gly Leu Leu Cys Ala  
115 120 125

Ala Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Glu Ser Asp  
130 135 140

His Lys Lys  
145

**PF 54195**

<210> 7  
<211> 169  
<212> PRT  
<213> Canola

<220>

<221> misc\_feature

<222> (1)...(169)

<223> unknown or other

<400> 7

Gly Ile Pro Gly Xaa Thr Phe Arg Gly Asp Val Ala Lys Ser His Gly  
1 5 10 15

Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn Ala Ser Val Ala  
20 25 30

Leu Gly Val Pro Val His Arg Leu Val Lys Ala Ala Asp Ser Val Ser  
35 40 45

Val Cys Ile Ser Lys Gly Leu Gly Ala Pro Val Gly Ser Val Ile Val  
50 55 60

Gly Ser Thr Ala Phe Ile Glu Lys Ala Lys Ile Leu Thr Lys Thr Leu  
65 70 75 80

Gly Gly Gly Met Arg Gln Val Gly Ile Leu Cys Ala Ala Tyr Val  
85 90 95

Ala Val Arg Asp Thr Val Gly Lys Leu Ala Asp Asp His Arg Arg Ala  
100 105 110

Lys Val Leu Ala Asp Gly Leu Lys Lys Ile Lys His Phe Arg Val Asp  
115 120 125

Thr Thr Ser Val Glu Thr Asn Met Val Phe Phe Asp Ile Val Asp Ser  
130 135 140

Arg Ile Ser Pro Asp Lys Leu Cys Gln Val Leu Glu Gln Arg Asn Val  
145 150 155 160

Leu Ala Met Pro Ala Gly Ser Lys Arg  
165

**PF 54195**

<210> 8  
<211> 362  
<212> PRT  
<213> Canola

<400> 8

Ile Glu Ile Lys Met Val Met Arg Thr Val Asp Leu Arg Ser Asp Thr  
1 5 10 15

Val Thr Arg Pro Thr Asp Ala Met Arg Glu Ala Met Gly Ser Ala Glu  
20 25 30

Val Asp Asp Asp Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu  
35 40 45

Glu Glu Ile Ala Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro  
50 55 60

Ser Gly Thr Met Gly Asn Leu Ile Cys Val Met Val His Cys Asp Val  
65 70 75 80

Arg Gly Ser Glu Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr  
85 90 95

Glu Asn Gly Gly Ile Ser Thr Ile Gly Gly Val His Pro Lys Thr Ile  
100 105 110

Lys Asn Glu Glu Asp Gly Thr Met Asp Leu Gly Ala Ile Glu Ala Ala  
115 120 125

Ile Arg Asp Pro Lys Gly Ser Thr Phe Tyr Pro Ser Thr Arg Leu Ile  
130 135 140

Cys Leu Glu Asn Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Ala  
145 150 155 160

Glu Tyr Thr Asp Arg Val Gly Glu Ile Ala Lys Arg His Gly Leu Lys  
165 170 175

Leu His Ile Asp Gly Ala Arg Leu Phe Asn Ala Ser Ile Ala Leu Gly  
180 185 190

Val Pro Val His Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys  
195 200 205

Leu Ser Lys Gly Leu Gly Ala Pro Ile Gly Ser Val Val Val Gly Ser  
210 215 220

Gln Ser Phe Ile Glu Lys Ala Lys Thr Leu Arg Lys Thr Leu Gly Gly  
225 230 235 240

Gly Met Arg Gln Ile Gly Val Leu Cys Ala Ala Ala Leu Val Ala Leu  
245 250 255

Gln Glu Asn Leu Pro Lys Leu Gln Phe Asp His Lys Lys Thr Lys Leu  
260 265 270

Leu Ala Glu Gly Leu Asn Gln Met Lys Gly Ile Arg Val Asn Val Ala  
275 280 285

**PF 54195**

Ala Met Glu Thr Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys  
290 295 300

Leu Thr Ala Glu Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu  
305 310 315 320

Val Ile Pro Glu Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln  
325 330 335

Ile Thr Thr Ser Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala  
340 345 350

Val Gln Thr Ile His Glu Pro Cys Gln Asn  
355 360

<210> 9  
<211> 196  
<212> PRT  
<213> Canola

<400> 9

Gly Phe Leu Leu Lys His Lys Tyr Ile Tyr Tyr Cys Cys Tyr Leu Phe  
1 5 10 15

Glu Ser Lys Ser Asn Asn Phe Leu Phe Ser Val Ile Lys Met Val Thr  
20 25 30

Pro Val Ile Arg Thr Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro  
35 40 45

Thr Glu Ser Met Arg Ser Ala Met Ala Asn Ala Glu Val Asp Asp Asp  
50 55 60

Val Leu Gly Asn Asp Pro Thr Ala Val Leu Leu Glu Arg Glu Val Ala  
65 70 75 80

Glu Ile Ala Gly Lys Glu Ala Ala Met Phe Val Pro Ser Gly Thr Met  
85 90 95

Gly Asn Leu Ile Ser Val Leu Val His Cys Asp Glu Arg Gly Ser Glu  
100 105 110

Val Ile Leu Gly Asp Asp Ser His Ile His Ile Tyr Glu Asn Gly Gly  
115 120 125

Val Ser Ser Leu Gly Gly Val His Pro Arg Thr Val Lys Asn Glu Glu  
130 135 140

Asp Gly Thr Met Glu Ile Ser Ser Ile Glu Ala Ala Val Arg Ser Pro  
145 150 155 160

Thr Gly Asp Leu His Tyr Pro Val Thr Lys Leu Ile Cys Leu Glu Asn  
165 170 175

Thr Gln Ala Asn Cys Gly Gly Arg Cys Leu Pro Ile Glu Tyr Ile Asp  
180 185 190

Lys Val Gly Glu  
195

<210> 10  
<211> 104  
<212> PRT  
<213> Soybean

<400> 10

Ile	Gly	Ile	Lys	Met	Val	Met	Arg	Ile	Val	Asp	Leu	Arg	Ser	Asp	Thr
1				5				10					15		

Val	Thr	Arg	Pro	Thr	Asp	Ala	Met	Arg	Glu	Ala	Met	Ala	Ser	Ala	Glu
	20				25							30			

Val	Asp	Asp	Asp	Val	Leu	Gly	Tyr	Asp	Pro	Thr	Ala	Arg	Gly	Leu	Glu
	35					40				45					

Glu	Glu	Met	Ala	Lys	Met	Met	Gly	Lys	Glu	Ala	Ala	Leu	Phe	Val	Pro
	50				55				60						

Ser	Gly	Thr	Met	Gly	Asn	Leu	Ile	Cys	Val	Met	Val	His	Cys	Asp	Val
65			70					75				80			

Arg	Gly	Ser	Glu	Val	Ile	Leu	Gly	Asp	Thr	Cys	His	Ile	His	Val	Tyr
	85						90				95				

Glu	Asn	Gly	Gly	Ile	Ser	Thr	Ile								
				100											

<210> 11  
<211> 738  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)...(738)  
<223> Protein similar to lysine decarboxylase

<400> 11

atg	aca	atg	gaa	aaa	aat	gga	ggg	aat	agc	agc	cgt	ggg	ggc	caa	gtt
Met															48
1						5			10				15		

ggc	ggc	aag	tct	gtg	tgt	gtt	tac	tgc	ggg	tct	tca	ttt	ggc	gct	aag
Gly	Gly	Lys	Ser	Val	Cys	Val	Tyr	Cys	Gly	Ser	Ser	Phe	Gly	Ala	Lys
						20			25			30			96

gcg	cta	tac	tca	gaa	agt	gca	gaa	tta	gga	gcc	ctt	ttc	cat	aag	
Ala															144
Leu	Tyr	Ser	Glu	Ser	Ala	Glu	Glu	Leu	Gly	Ala	Leu	Phe	His	Lys	
					35			40		45					

## PF 54195

ctg gga tgg aaa ttg gta tac ggt gga ggc act act ggt ttg atg ggc Leu Gly Trp Lys Leu Val Tyr Gly Gly Thr Thr Gly Leu Met Gly 50 55 60	192
aag ata gca agg tct acg atg gga cct gat tta agc gga cag gtt cac Lys Ile Ala Arg Ser Thr Met Gly Pro Asp Leu Ser Gly Gln Val His 65 70 75 80	240
ggt atc att cca aat gca ctt gtg tct aag gaa agg aca gac gag gat Gly Ile Ile Pro Asn Ala Leu Val Ser Lys Glu Arg Thr Asp Glu Asp 85 90 95	288
aaa gaa gat gtt aat aaa gca ttg ttg gag tct gta gaa aat cat aag Lys Glu Asp Val Asn Lys Ala Leu Leu Glu Ser Val Glu Asn His Lys 100 105 110	336
ggc gcc act cct att tct gaa gag tat ggg gaa aca acg att gta cca Gly Ala Thr Pro Ile Ser Glu Glu Tyr Gly Glu Thr Thr Ile Val Pro 115 120 125	384
gat atg cat acg aga aaa aga atg atg gca aat ttg agt gac gcg ttt Asp Met His Thr Arg Lys Arg Met Met Ala Asn Leu Ser Asp Ala Phe 130 135 140	432
gtt gct atg cct ggt gga tac ggg act ttt gaa gaa atc atg gaa tgt Val Ala Met Pro Gly Gly Tyr Gly Thr Phe Glu Glu Ile Met Glu Cys 145 150 155 160	480
atc acg tgg tcg caa ctg ggg att cat aat aaa cca att atc ttg ttc Ile Thr Trp Ser Gln Leu Gly Ile His Asn Lys Pro Ile Ile Leu Phe 165 170 175	528
aat atc gat ggg ttc tat gac aaa tta ttg gag ttc ctc aaa cac tct Asn Ile Asp Gly Phe Tyr Asp Lys Leu Leu Glu Phe Leu Lys His Ser 180 185 190	576
att caa gaa cgg ttc atc agt gtg aag aat ggt gaa atc att caa gtt Ile Gln Glu Arg Phe Ile Ser Val Lys Asn Gly Glu Ile Ile Gln Val 195 200 205	624
gcc tcc act ccg cag gaa gtt gtt gat aaa ata gag aag tac gtc gtt Ala Ser Thr Pro Gln Glu Val Val Asp Lys Ile Glu Lys Tyr Val Val 210 215 220	672
cca gag ggc cgt ttc aat ttg aat tgg agc gac gaa ggt cac gct cac Pro Glu Gly Arg Phe Asn Leu Asn Trp Ser Asp Glu Gly His Ala His 225 230 235 240	720
gag gat tgt gct aaa taa Glu Asp Cys Ala Lys 245	738

<210> 12  
<211> 245  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 12

Met Thr Met Glu Lys Asn Gly Gly Asn Ser Ser Arg Gly Gly Gln Val 1 5 10 15
--

Gly Gly Lys Ser Val Cys Val Tyr Cys Gly Ser Ser Phe Gly Ala Lys  
 20 25 30

Ala Leu Tyr Ser Glu Ser Ala Glu Glu Leu Gly Ala Leu Phe His Lys  
 35 40 45

Leu Gly Trp Lys Leu Val Tyr Gly Gly Thr Thr Gly Leu Met Gly  
 50 55 60

Lys Ile Ala Arg Ser Thr Met Gly Pro Asp Leu Ser Gly Gln Val His  
 65 70 75 80

Gly Ile Ile Pro Asn Ala Leu Val Ser Lys Glu Arg Thr Asp Glu Asp  
 85 90 95

Lys Glu Asp Val Asn Lys Ala Leu Leu Glu Ser Val Glu Asn His Lys  
 100 105 110

Gly Ala Thr Pro Ile Ser Glu Glu Tyr Gly Glu Thr Thr Ile Val Pro  
 115 120 125

Asp Met His Thr Arg Lys Arg Met Met Ala Asn Leu Ser Asp Ala Phe  
 130 135 140

Val Ala Met Pro Gly Gly Tyr Gly Thr Phe Glu Glu Ile Met Glu Cys  
 145 150 155 160

Ile Thr Trp Ser Gln Leu Gly Ile His Asn Lys Pro Ile Ile Leu Phe  
 165 170 175

Asn Ile Asp Gly Phe Tyr Asp Lys Leu Leu Glu Phe Leu Lys His Ser  
 180 185 190

Ile Gln Glu Arg Phe Ile Ser Val Lys Asn Gly Glu Ile Ile Gln Val  
 195 200 205

Ala Ser Thr Pro Gln Glu Val Val Asp Lys Ile Glu Lys Tyr Val Val  
 210 215 220

Pro Glu Gly Arg Phe Asn Leu Asn Trp Ser Asp Glu Gly His Ala His  
 225 230 235 240

Glu Asp Cys Ala Lys  
 245

<210> 13  
 <211> 1083  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS  
 <222> (1)..(1083)  
 <223> Threonine aldolase

<400>	13		
atg gta act aga att gtg gat ctt cggtca gac aca gtt aca aag cca			48
Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro			
1	5	10	15
act gaa gca atg aga gct gct atg gca agt gct gaa gtt gat gac gat			96
Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp			
20	25	30	
gtt cta ggc tat gat cca act gct ttt cgc tta gaa aca gag atg gca			144
Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala			
35	40	45	
aag aca atg ggc aaa gaa gct gct ctt ttt gtt cca tct ggc act atg			192
Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met			
50	55	60	
ggg aac ctt gta tct gta ctt gtt cat tgt gat gtc agg gga agt gag			240
Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu			
65	70	75	80
gtt att ctt gga gac aat tgc cat atc aac att ttt gag aat gga ggc			288
Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly			
85	90	95	
att gca acc att ggg gga gtg cat cca aga caa gtg aaa aat aac gat			336
Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp			
100	105	110	
gat gga acc atg gac att gat ttg att gag gct gct atc agg gac cca			384
Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro			
115	120	125	
atg ggg gag cta ttc tat cca acc acc aag ctt att tgc ttg gaa aat			432
Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn			
130	135	140	
act cat gca aac tct ggt ggc aga tgc ctc tca gtt gaa tat aca gac			480
Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp			
145	150	155	160
aga gtt gga gag tta gct aag aag cat gga ctg aag ctt cac att gat			528
Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp			
165	170	175	
ggg gcc cgt att ttt aac gca tca gtt gca ctt ggt gtt cca gtg gat			576
Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp			
180	185	190	
agg ctt gtc cag gcg gct gat tca gtt tcc gtt tgc cta tct aaa ggt			624
Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly			
195	200	205	
ata ggt gct cca gtt gga tct gtt att gtt ggt tcc aag aat ttt att			672
Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile			
210	215	220	
gcc aag gct aga cga ctc cgg aaa acc tta gga ggt gga atg aga cag			720
Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln			
225	230	235	240
att ggc ctc ctt tgt gcc gct gca ctt gtt gcc ttg cag gaa aat gtt			768

## PF 54195

Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val			
245	250	255	
ggg aag ctg gaa agt gat cac aag aaa gct aga ctt ttg gct gat gga		816	
Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly			
260	265	270	
tta aac gaa gtt aaa gga ttg aga gtg gat gcc tgc tct gtg gag acc		864	
Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr			
275	280	285	
aat atg gta ttt att gac att gaa gag ggt aca aag act aga gca gaa		912	
Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu			
290	295	300	
aag ata tgc aag tac atg gaa gaa cgt ggt atc ctt gtg atg caa gag		960	
Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu			
305	310	315	320
agt tca tca aga atg aga gtt gtt ctc cat cac caa ata tca gca agt		1008	
Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser			
325	330	335	
gat gtg caa tat gcc ttg tcg tgc ttt cag caa gct cta gct gtc aaa		1056	
Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys			
340	345	350	
gga gta caa aag gaa atg ggc aac taa		1083	
Gly Val Gln Lys Glu Met Gly Asn			
355	360		
<210> 14			
<211> 360			
<212> PRT			
<213> Glycine max			
<400> 14			
Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro			
1	5	10	15
Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp			
20	25	30	
Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala			
35	40	45	
Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met			
50	55	60	
Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu			
65	70	75	80
Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly			
85	90	95	
Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp			
100	105	110	

Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro  
 115 120 125

Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn  
 130 135 140

Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp  
 145 150 155 160

Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp  
 165 170 175

Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp  
 180 185 190

Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly  
 195 200 205

Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile  
 210 215 220

Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Met Arg Gln  
 225 230 235 240

Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val  
 245 250 255

Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly  
 260 265 270

Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr  
 275 280 285

Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu  
 290 295 300

Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu  
 305 310 315 320

Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser  
 325 330 335

Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys  
 340 345 350

Gly Val Gln Lys Glu Met Gly Asn  
 355 360

<210> 15  
 <211> 1077  
 <212> DNA  
 <213> Brassica napus

<220>  
 <221> CDS  
 <222> (1)...(1077)  
 <223> Threonine aldolase

<400>	15															
atg	gtg	atg	cga	act	gtg	gat	cta	cgg	tca	gac	acc	gtg	act	aga	cct	48
Met	Val	Met	Arg	Thr	Val	Asp	Leu	Arg	Ser	Asp	Thr	Val	Thr	Arg	Pro	
1		5				10							15			
acc	gat	gcc	atg	cgt	gaa	gca	atg	gga	agc	gca	gaa	gta	gac	gat	gac	96
Thr	Asp	Ala	Met	Arg	Glu	Ala	Met	Gly	Ser	Ala	Glu	Val	Asp	Asp	Asp	
20			25								30					
gtc	ctc	ggc	tac	gac	cca	acg	gct	cga	cgt	ctt	gaa	gag	gag	ata	gcc	144
Val	Leu	Gly	Tyr	Asp	Pro	Thr	Ala	Arg	Arg	Leu	Glu	Glu	Glu	Ile	Ala	
35				40						45						
aag	atg	atg	ggg	aaa	gaa	gca	gct	ctc	ttc	gtg	cca	tct	ggt	aca	atg	192
Lys	Met	Met	Gly	Lys	Glu	Ala	Ala	Leu	Phe	Val	Pro	Ser	Gly	Thr	Met	
50			55							60						
ggg	aac	ctc	ata	tgc	gtt	atg	gtt	cac	tgc	gac	gtg	aga	ggc	agc	gag	240
Gly	Asn	Leu	Ile	Cys	Val	Met	Val	His	Cys	Asp	Val	Arg	Gly	Ser	Glu	
65			70					75			80					
gtg	att	ctt	gga	gac	aac	tgt	cac	atc	cat	gtc	tac	gag	aac	gga	ggg	288
Val	Ile	Leu	Gly	Asp	Asn	Cys	His	Ile	His	Val	Tyr	Glu	Asn	Gly	Gly	
85			90							95						
ata	tca	acg	ata	gga	ggc	gtg	cat	ccc	aag	aca	atc	aag	aat	gaa	gaa	336
Ile	Ser	Thr	Ile	Gly	Gly	Val	His	Pro	Lys	Thr	Ile	Lys	Asn	Glu	Glu	
100			105						110							
gac	ggg	aca	atg	gac	ttg	ggg	gct	ata	gaa	gca	gct	att	aga	gat	cct	384
Asp	Gly	Thr	Met	Asp	Leu	Gly	Ala	Ile	Glu	Ala	Ala	Ile	Arg	Asp	Pro	
115				120					125							
aaa	gga	agc	acg	ttt	tat	cca	tca	aca	agg	ttg	att	tgt	ttg	gag	aac	432
Lys	Gly	Ser	Thr	Phe	Tyr	Pro	Ser	Thr	Arg	Leu	Ile	Cys	Leu	Glu	Asn	
130			135						140							
aca	cat	gcc	aac	tct	ggg	aga	tgt	ttg	agt	gcg	gaa	tac	aca	gat	480	
Thr	His	Ala	Asn	Ser	Gly	Gly	Arg	Cys	Leu	Ser	Ala	Glu	Tyr	Thr	Asp	
145			150					155			160					
aga	gtt	gga	gag	att	gcc	aag	aga	cat	gga	tta	aag	ctt	cat	atc	gat	528
Arg	Val	Gly	Glu	Ile	Ala	Lys	Arg	His	Gly	Leu	Lys	Leu	His	Ile	Asp	
165			170						175							
gga	gct	cgc	ctt	ttt	aat	gct	att	gca	ctt	gga	gtt	cca	gtc	cat	576	
Gly	Ala	Arg	Leu	Phe	Asn	Ala	Ser	Ile	Ala	Leu	Gly	Val	Pro	Val	His	
180				185					190							
agg	ctt	gta	cag	gct	gct	gac	tct	gtt	tcg	gtg	tgt	ctc	tct	aaa	ggt	624
Arg	Leu	Val	Gln	Ala	Ala	Asp	Ser	Val	Ser	Val	Cys	Leu	Ser	Lys	Gly	
195			200						205							
ctt	gga	gct	cca	ata	gga	tct	gta	gtc	gtt	ggt	tca	cag	agt	ttc	ata	672
Leu	Gly	Ala	Pro	Ile	Gly	Ser	Val	Val	Val	Gly	Ser	Gln	Ser	Phe	Ile	
210			215						220							
gaa	aag	gcg	aaa	acg	tta	aga	aaa	aca	tta	ggt	gga	gga	atg	aga	caa	720
Glu	Lys	Ala	Lys	Thr	Leu	Arg	Lys	Thr	Leu	Gly	Gly	Gly	Met	Arg	Gln	
225			230						235			240				

## PF 54195

ata ggc gtc ctg tgc gca gcc gct ttg gtc gca ctt caa gag aat ctc Ile Gly Val Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Leu 245 250 255	768
cca aag tta caa ttt gac cac aag aag aca aaa ttg tta gct gaa ggg Pro Lys Leu Gln Phe Asp His Lys Lys Thr Lys Leu Leu Ala Glu Gly 260 265 270	816
ttg aat caa atg aaa ggg att aga gtg aac gtt gca gcc atg gag acc Leu Asn Gln Met Lys Gly Ile Arg Val Asn Val Ala Ala Met Glu Thr 275 280 285	864
aac atg ata ttc atg gat atg gag gat gga tca aaa ctg acc gct gaa Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys Leu Thr Ala Glu 290 295 300	912
aaa ctc cgc aag agt cta acg gag cat ggc att ctc gtc atc cct gaa Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu Val Ile Pro Glu 305 310 315 320	960
aac tct acc cga atc aga atg gtt cta cac cac cag ata aca aca agt Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln Ile Thr Thr Ser 325 330 335	1008
gat gtg cat tac aca ttg tct tgc tta caa caa gca gtg cag acg att Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala Val Gln Thr Ile 340 345 350	1056
cat gaa cca tgc caa aac taa His Glu Pro Cys Gln Asn 355	1077

<210> 16  
<211> 358  
<212> PRT  
<213> Brassica napus

<400> 16	
Met Val Met Arg Thr Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro 1 5 10 15	
Thr Asp Ala Met Arg Glu Ala Met Gly Ser Ala Glu Val Asp Asp Asp 20 25 30	
Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Ile Ala 35 40 45	
Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met 50 55 60	
Gly Asn Leu Ile Cys Val Met Val His Cys Asp Val Arg Gly Ser Glu 65 70 75 80	
Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly 85 90 95	
Ile Ser Thr Ile Gly Gly Val His Pro Lys Thr Ile Lys Asn Glu Glu 100 105 110	

**PF 54195**

Asp Gly Thr Met Asp Leu Gly Ala Ile Glu Ala Ala Ile Arg Asp Pro  
115 120 125

Lys Gly Ser Thr Phe Tyr Pro Ser Thr Arg Leu Ile Cys Leu Glu Asn  
130 135 140

Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Ala Glu Tyr Thr Asp  
145 150 155 160

Arg Val Gly Glu Ile Ala Lys Arg His Gly Leu Lys Leu His Ile Asp  
165 170 175

Gly Ala Arg Leu Phe Asn Ala Ser Ile Ala Leu Gly Val Pro Val His  
180 185 190

Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly  
195 200 205

Leu Gly Ala Pro Ile Gly Ser Val Val Val Gly Ser Gln Ser Phe Ile  
210 215 220

Glu Lys Ala Lys Thr Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln  
225 230 235 240

Ile Gly Val Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Leu  
245 250 255

Pro Lys Leu Gln Phe Asp His Lys Lys Thr Lys Leu Leu Ala Glu Gly  
260 265 270

Leu Asn Gln Met Lys Gly Ile Arg Val Asn Val Ala Ala Met Glu Thr  
275 280 285

Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys Leu Thr Ala Glu  
290 295 300

Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu Val Ile Pro Glu  
305 310 315 320

Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln Ile Thr Thr Ser  
325 330 335

Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala Val Gln Thr Ile  
340 345 350

His Glu Pro Cys Gln Asn  
355

<210> 17  
<211> 570  
<212> DNA  
<213> Glycine max

<220>  
<221> CDS  
<222> (1)...(570)  
<223> Lysine decarboxylase

## PF 54195

<400> 17  
atg gaa ata agg gtt tca aag ttc aag agg att tgt gtc ttc tgt ggg 48  
Met Glu Ile Arg Val Ser Lys Phe Lys Arg Ile Cys Val Phe Cys Gly  
1 5 10 15

agt agc cct ggc aaa aag aga agc tac caa gat gct gcc att gaa ctt 96  
Ser Ser Pro Gly Lys Lys Arg Ser Tyr Gln Asp Ala Ala Ile Glu Leu  
20 25 30

ggc aat gaa ttg gtc tca agg aac att gat ctg gtg tat gga ggg gga 144  
Gly Asn Glu Leu Val Ser Arg Asn Ile Asp Leu Val Tyr Gly Gly Gly  
35 40 45

agc att ggt cta atg ggt tta gtt tca caa gct gtt cat gat ggc ggt 192  
Ser Ile Gly Leu Met Gly Leu Val Ser Gln Ala Val His Asp Gly Gly  
50 55 60

cgg cat gtc atc gga gtt att ccc aag acc ctc atg cct cga gag cta 240  
Arg His Val Ile Gly Val Ile Pro Lys Thr Leu Met Pro Arg Glu Leu  
65 70 75 80

act ggt gaa aca gtg gga gaa gta aaa gct gtt gct gat atg cac caa 288  
Thr Gly Glu Thr Val Gly Glu Val Lys Ala Val Ala Asp Met His Gln  
85 90 95

agg aag gca gag atg gcc aag cat tca gac gcc ttt att gcc tta cca 336  
Arg Lys Ala Glu Met Ala Lys His Ser Asp Ala Phe Ile Ala Leu Pro  
100 105 110

ggt gga tat ggg act cta gag gag ctt ctt gaa gtc ata acc tgg gca 384  
Gly Gly Tyr Gly Thr Leu Glu Glu Leu Leu Glu Val Ile Thr Trp Ala  
115 120 125

caa ctt ggg att cat gac aag ccg gtg gga tta gta aat gtt gat gga 432  
Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu Val Asn Val Asp Gly  
130 135 140

tac ttt aat tcc ttg ctg tca ttt att gac aaa gct gtg gaa gag gga 480  
Tyr Phe Asn Ser Leu Leu Ser Phe Ile Asp Lys Ala Val Glu Glu Gly  
145 150 155 160

ttt atc agt cca aat gct cgc cac ata att gta tca gca ccc aca gca 528  
Phe Ile Ser Pro Asn Ala Arg His Ile Ile Val Ser Ala Pro Thr Ala  
165 170 175

aaa gag ttg gtg aag aaa ttg gag gat tac gtt ccc tgt taa 570  
Lys Glu Leu Val Lys Lys Leu Glu Asp Tyr Val Pro Cys  
180 185

<210> 18  
<211> 189  
<212> PRT  
<213> Glycine max

<400> 18

Met Glu Ile Arg Val Ser Lys Phe Lys Arg Ile Cys Val Phe Cys Gly  
1 5 10 15

Ser Ser Pro Gly Lys Lys Arg Ser Tyr Gln Asp Ala Ala Ile Glu Leu  
 20 25 30  
 Gly Asn Glu Leu Val Ser Arg Asn Ile Asp Leu Val Tyr Gly Gly Gly  
 35 40 45  
 Ser Ile Gly Leu Met Gly Leu Val Ser Gln Ala Val His Asp Gly Gly  
 50 55 60  
 Arg His Val Ile Gly Val Ile Pro Lys Thr Leu Met Pro Arg Glu Leu  
 65 70 75 80  
 Thr Gly Glu Thr Val Gly Glu Val Lys Ala Val Ala Asp Met His Gln  
 85 90 95  
 Arg Lys Ala Glu Met Ala Lys His Ser Asp Ala Phe Ile Ala Leu Pro  
 100 105 110  
 Gly Gly Tyr Gly Thr Leu Glu Glu Leu Leu Glu Val Ile Thr Trp Ala  
 115 120 125  
 Gin Leu Gly Ile His Asp Lys Pro Val Gly Leu Val Asn Val Asp Gly  
 130 135 140  
 Tyr Phe Asn Ser Leu Leu Ser Phe Ile Asp Lys Ala Val Glu Glu Gly  
 145 150 155 160  
 Phe Ile Ser Pro Asn Ala Arg His Ile Ile Val Ser Ala Pro Thr Ala  
 165 170 175  
 Lys Glu Leu Val Lys Lys Leu Glu Asp Tyr Val Pro Cys  
 180 185

<210> 19  
 <211> 675  
 <212> DNA  
 <213> *Hordeum vulgare*

<220>  
 <221> CDS  
 <222> (1)...(675)  
 <223> Lysine decarboxylase

<400> 19  
 atg ggc gac acc acc gcg ccc tcg ccg ccg agg agg ttc ggc agg atc 48  
 Met Gly Asp Thr Thr Ala Pro Ser Pro Pro Arg Arg Phe Gly Arg Ile  
 1 5 10 15  
 tgc gtc ttc tg`c ggc agg aac tcc ggc aac cgc gcc gtg ttc ggc gac 96  
 Cys Val Phe Cys Gly Arg Asn Ser Gly Asn Arg Ala Val Phe Gly Asp  
 20 25 30

## PF 54195

gcc gcg ctc gag ctc ggc cag ggc ctg gtg acg agg ggg gtc gat ctg Ala Ala Leu Glu Leu Gly Gln Gly Leu Val Thr Arg Gly Val Asp Leu 35 40 45	144
gtc tac ggc ggc agt atc ggg ctg atg ggc ctg atc gcg cag acg Val Tyr Gly Gly Ser Ile Gly Leu Met Gly Leu Ile Ala Gln Thr 50 55 60	192
gtt ctc gac ggc ggc tgc cgc gtc ctc ggg gtg att cca aga gca ctc Val Leu Asp Gly Gly Cys Arg Val Leu Gly Val Ile Pro Arg Ala Leu 65 70 75 80	240
atg ccc ctc gag ata tcc ggt gca agt gtt gga gaa gta aag att gtc Met Pro Leu Glu Ile Ser Gly Ala Ser Val Gly Glu Val Lys Ile Val 85 90 95	288
tcc gac atg cat gag agg aaa gct gag atg gcg cga caa gcc gat gca Ser Asp Met His Glu Arg Lys Ala Glu Met Ala Arg Gln Ala Asp Ala 100 105 110	336
ttc att gct ctt ccg ggt ggg tat gga aca atg gaa gag ctg gta gag Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met Glu Glu Leu Val Glu 115 120 125	384
atg atc act tgg tcg cag ctt gga atc cat gac aaa ccg gtc ggg ttg Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu 130 135 140	432
cta aac gtc gat ggg tac tat gat ccg tta ctc gcg ctg ttc gac aag Leu Asn Val Asp Gly Tyr Asp Pro Leu Leu Ala Leu Phe Asp Lys 145 150 155 160	480
ggc gcg ggg gaa ggg ttt ttt aag gcc gat tgc agg ccg ata atc gtg Gly Ala Gly Glu Phe Lys Ala Asp Cys Arg Pro Ile Ile Val 165 170 175	528
tcg gca cca act gcc cac gaa ctg ctg aca aaa atg gag caa tac acc Ser Ala Pro Thr Ala His Glu Leu Leu Thr Lys Met Glu Gln Tyr Thr 180 185 190	576
cgt tca ccc ccg gag gtg gcc tcg ccg acg acg tgg gag atg acc gag Arg Ser Pro Arg Glu Val Ala Ser Arg Thr Ser Trp Glu Met Thr Glu 195 200 205	624
atg ggc tcc ggg aaa gca ccg gag ccg gag gag gag gcg gcg gca tcg Met Gly Ser Gly Lys Ala Pro Glu Pro Glu Glu Ala Ala Ala Ser 210 215 220	672
taa	675

<210> 20  
<211> 224  
<212> PRT  
<213> Hordeum vulgare

<400> 20

Met Gly Asp Thr Thr Ala Pro Ser Pro Pro Arg Arg Phe Gly Arg Ile 1 5 10 15
--

Cys Val Phe Cys Gly Arg Asn Ser Gly Asn Arg Ala Val Phe Gly Asp  
 20 25 30

Ala Ala Leu Glu Leu Gly Gln Gly Leu Val Thr Arg Gly Val Asp Leu  
 35 40 45

Val Tyr Gly Gly Ser Ile Gly Leu Met Gly Leu Ile Ala Gln Thr  
 50 55 60

Val Leu Asp Gly Gly Cys Arg Val Leu Gly Val Ile Pro Arg Ala Leu  
 65 70 75 80

Met Pro Leu Glu Ile Ser Gly Ala Ser Val Gly Glu Val Lys Ile Val  
 85 90 95

Ser Asp Met His Glu Arg Lys Ala Glu Met Ala Arg Gln Ala Asp Ala  
 100 105 110

Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met Glu Glu Leu Val Glu  
 115 120 125

Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu  
 130 135 140

Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu Ala Leu Phe Asp Lys  
 145 150 155 160

Gly Ala Gly Glu Gly Phe Phe Lys Ala Asp Cys Arg Pro Ile Ile Val  
 165 170 175

Ser Ala Pro Thr Ala His Glu Leu Leu Thr Lys Met Glu Gln Tyr Thr  
 180 185 190

Arg Ser Pro Arg Glu Val Ala Ser Arg Thr Ser Trp Glu Met Thr Glu  
 195 200 205

Met Gly Ser Gly Lys Ala Pro Glu Pro Glu Glu Ala Ala Ala Ser  
 210 215 220

<210> 21  
<211> 717  
<212> DNA  
<213> artificial

<220>  
<221> CDS  
<222> (1)...(717)  
<223> Lysine decarboxylase

<400> 21  
atg gag gag aat caa gag aag ttt gct ccg gag agc agc ggc ggc gac  
Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp  
1 5 10 15

ggt ggt ggc tcg gtg aga acg atc tgc gtc ttc tgc ggc agc agg ccg Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro	96
20 25 30	
ggg aac cgg ccg tcc ttc agc gct gcg ggc ctc gac ctg ggg aag cag Gly Asn Arg Pro Ser Phe Ser Ala Ala Leu Asp Leu Gly Lys Gln	144
35 40 45	
ctg gtc gag agg cag atg aac ctg gtg tac ggc ggc agc ggc ggg Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Ser Gly Gly	192
50 55 60	
ctg atg ggc ctg gtg tcc aag gcc gtc tac gaa ggc ggc cgc cac gtc Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val	240
65 70 75 80	
ctc ggg gtc atc cct acc gcc ctc cta cct gaa gag gtg tca ggg gag Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu	288
85 90 95	
aca ttg gga gag gtg aaa gtg gtc agg gac atg cat cag cgc aag gcg Thr Leu Gly Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala	336
100 105 110	
gaa atg gcg aaa cat gcc gac gct ttc atc gcc ctg cca ggt ggt tac Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr	384
115 120 125	
ggg aca atc gaa gaa ctg ctg gag atc ata gcg tgg gcg cag ctg ggc Gly Thr Ile Glu Glu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly	432
130 135 140	
atc cac agc aaa ccg gtg ggg ttg ctc aac gtg gac ggc tac tac aac Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn	480
145 150 155 160	
agc ctg ctc tcg ttc gac aag gct gtc gag gag ggc ttc atc gac Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp	528
165 170 175	
acc aag gca ccg aac atc ttc gtc ctc gct gac acc gcc gcc gac ctg Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu	576
180 185 190	
ctg act agg ctc acc atg atg gcg cgc ctg gca gcc gac gac gac gat Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp	624
195 200 205	
gct act act acc ccc aga gga gac gga gac gga gac gaa cac Ala Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Glu His	672
210 215 220	
aag ggg gcc acc acc gct gca ggc gtc aaa agg aaa agg ggc taa Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly	717
225 230 235	

**PF 54195**

<210> 22  
<211> 238  
<212> PRT  
<213> artificial

<400> 22

Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp  
1 5 10 15

Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro  
20 25 30

Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln  
35 40 45

Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Ser Gly Gly  
50 55 60

Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val  
65 70 75 80

Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu  
85 90 95

Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala  
100 105 110

Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr  
115 120 125

Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly  
130 135 140

Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn  
145 150 155 160

Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp  
165 170 175

Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu  
180 185 190

Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp  
195 200 205

Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Glu His  
210 215 220

Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly  
225 230 235

<210> 23  
<211> 717  
<212> DNA  
<213> Zea mays

PF 54195

<220>

<221> CDS

<222> (1)..(717)

<223> Lysine decarboxylase

<400> 23  
 atg gag gag aat caa gag aag ttt gct ccg gag agc agc ggc ggc gac  
 Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp  
 1 5 10 15  
 ggt ggt ggc tcg gtg aga acg atc tgc gtc ttc tgc ggc agc agg ccg  
 Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro  
 20 25 30  
 ggg aac cgg ccg tcc ttc agc gct gcg gcg ctc gac ctg ggg aag cag  
 Gly Asn Arg Pro Ser Phe Ser Ala Ala Leu Asp Leu Gly Lys Gln  
 35 40 45  
 ctg gtc gag agg cag atg aac ctg gtg tac ggc ggc ggc agc ggc ggg  
 Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Ser Gly Gly  
 50 55 60  
 ctg atg ggc ctg gtg tcc aag gcc gtc tac gaa ggc ggc cgc cac gtc  
 Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Arg His Val  
 65 70 75 80  
 ctc ggg gtc atc cct acc gcc ctc cta cct gaa gag gtg tca ggg gag  
 Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu  
 85 90 95  
 aca ttg gga gag gtg aaa gtg gtc agg gac atg cat cag cgc aag gcg  
 Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala  
 100 105 110  
 gaa atg gcg aaa cat gcc gac gct ttc atc gcc ctg cca ggt ggt tac  
 Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr  
 115 120 125  
 ggg aca atc gaa gaa ctg ctg gag atc ata gcg tgg gcg cag ctg ggc  
 Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly  
 130 135 140  
 atc cac agc aaa ccg gtg ggg ttg ctc aac gtg gac ggc tac tac aac  
 Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn  
 145 150 155 160  
 agc ctg ctc tcg ctg ttc gac aag gct gtc gag gag ggc ttc atc gac  
 Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp  
 165 170 175  
 acc aag gca cgg aac atc ttc gtc ctc gct gac acc gcc gcc gac ctg  
 Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu  
 180 185 190  
 ctg act agg ctc acc atg atg gcg cgc ctg gca gcc gac gac gac gat  
 Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp  
 195 200 205

gct act act acc ccc aga gga gac gga gac gga gac gaa cac 672  
 Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Glu His  
 210 215 220

aag ggg gcc acc acc gct gca ggc gtc aaa agg aaa agg ggc taa 717  
 Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly  
 225 230 235

<210> 24  
 <211> 238  
 <212> PRT  
 <213> Zea mays

<400> 24

Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp  
 1 5 10 15

Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro  
 20 25 30

Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln  
 35 40 45

Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Ser Gly Gly  
 50 55 60

Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val  
 65 70 75 80

Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu  
 85 90 95

Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala  
 100 105 110

Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr  
 115 120 125

Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly  
 130 135 140

Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn  
 145 150 155 160

Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp  
 165 170 175

Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu  
 180 185 190

Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp  
 195 200 205

Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Glu His  
 210 215 220

Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly  
 225 230 235

PF 54195

<210> 25  
<211> 672  
<212> DNA  
<213> *Oryza sativa*

<220>

<221> CDS

<222> (1)..(672)

<223> Lysine decarboxylase

<400> 25  
 atg ggc gac aac agc gcc gcc gcg gcg gcc gtg gcc gcg ccc cgc ggc 48  
 Met Gly Asp Asn Ser Ala Ala Ala Ala Ala Val Ala Ala Pro Arg Gly  
 1 5 10 15  
  
 agg ttc ggc agg atc tgc gtc ttc tgc ggc agc aac gcc ggc aac cgc 96  
 Arg Phe Gly Arg Ile Cys Val Phe Cys Gly Ser Asn Ala Gly Asn Arg  
 20 25 30  
  
 gcg gtg ttc ggc gac gcg gcg ctc cag ctc ggg cag gag ctg gtg tcg 144  
 Ala Val Phe Gly Asp Ala Ala Leu Gln Leu Gly Gln Glu Leu Val Ser  
 35 40 45  
  
 aga ggg atc gag ttg gtc tac ggt ggc ggc agc gtc ggg ttg atg ggc 192  
 Arg Gly Ile Glu Leu Val Tyr Gly Gly Ser Val Gly Leu Met Gly  
 50 55 60  
  
 ttg atc gcg cag acg gtt ctt gat ggc ggc tgc ggt gtt ctc ggg gtg 240  
 Leu Ile Ala Gln Thr Val Leu Asp Gly Gly Cys Gly Val Leu Gly Val  
 65 70 75 80  
  
 att cca aaa gca ctt atg ccc acc gag ata tca ggt gca agt gtt gga 288  
 Ile Pro Lys Ala Leu Met Pro Thr Glu Ile Ser Gly Ala Ser Val Gly  
 85 90 95  
  
 gaa gtg aaa att gtg tct gac atg cat gag agg aaa gct gag atg gca 336  
 Glu Val Lys Ile Val Ser Asp Met His Glu Arg Lys Ala Glu Met Ala  
 100 105 110  
  
 cgc caa tcc gat gcc ttc atc gct ctt cct gga ggg tat gga aca atg 384  
 Arg Gln Ser Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met  
 115 120 125  
  
 gag gag ttg tta gag atg ata act tgg tcacaa ctt gga att cat gac 432  
 Glu Glu Leu Leu Glu Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp  
 130 135 140  
  
 aaa cca gtt ggg ttg ctg aat gtg gac ggt tac tat gat ccg ttg ctt 480  
 Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu  
 145 150 155 160  
  
 cgc cta ttt gat aag ggt gcg gca gaa gga ttt att aag gcc gat tgc 528  
 Ala Leu Phe Asp Lys Gly Ala Ala Glu Gly Phe Ile Lys Ala Asp Cys  
 165 170 175

**PF 54195**

aga caa ata att gtt tcg gca ccg act gcg cat gag ctg ctg aga aag 576  
Arg Gln Ile Ile Val Ser Ala Pro Thr Ala His Glu Leu Arg Lys  
180 185 190

atg gag caa tac act cgt tca cac cag gag gta gcg cca cgt aca agc 624  
Met Glu Gln Tyr Thr Arg Ser His Gln Glu Val Ala Pro Arg Thr Ser  
195 200 205

tgg gag atg tca gag ctt ggt tat gga aag aca cca gag gaa tcg taa 672  
Trp Glu Met Ser Glu Leu Gly Tyr Gly Lys Thr Pro Glu Glu Ser  
210 215 220

<210> 26  
<211> 223  
<212> PRT  
<213> Oryza sativa

<400> 26

Met Gly Asp Asn Ser Ala Ala Ala Ala Val Ala Ala Pro Arg Gly  
1 5 10 15

Arg Phe Gly Arg Ile Cys Val Phe Cys Gly Ser Asn Ala Gly Asn Arg  
20 25 30

Ala Val Phe Gly Asp Ala Ala Leu Gln Leu Gly Gln Glu Leu Val Ser  
35 40 45

Arg Gly Ile Glu Leu Val Tyr Gly Gly Ser Val Gly Leu Met Gly  
50 55 60

Leu Ile Ala Gln Thr Val Leu Asp Gly Gly Cys Gly Val Leu Gly Val  
65 70 75 80

Ile Pro Lys Ala Leu Met Pro Thr Glu Ile Ser Gly Ala Ser Val Gly  
85 90 95

Glu Val Lys Ile Val Ser Asp Met His Glu Arg Lys Ala Glu Met Ala  
100 105 110

Arg Gln Ser Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met  
115 120 125

Glu Glu Leu Leu Glu Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp  
130 135 140

Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu  
145 150 155 160

Ala Leu Phe Asp Lys Gly Ala Ala Glu Gly Phe Ile Lys Ala Asp Cys  
165 170 175

Arg Gln Ile Ile Val Ser Ala Pro Thr Ala His Glu Leu Arg Lys  
180 185 190

Met Glu Gln Tyr Thr Arg Ser His Gln Glu Val Ala Pro Arg Thr Ser  
195 200 205

Trp Glu Met Ser Glu Leu Gly Tyr Gly Lys Thr Pro Glu Glu Ser  
210 215 220